PCT09

RAW SEQUENCE LISTING DATE: 05/02/2002
PATENT APPLICATION: US/09/743,885A TIME: 17:07:38

Input Set : A:\743885seq.mar.txt
Output Set: N:\CRF3\05022002\I743885A.raw

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<110> APPLICANT: CREEMERS, Jantina
ANGENENT, Gerrit
KATER, Martin
<120> TITLE OF INVENTION: Process to collect metabolites from modified nectar by insects
<130> FILE REFERENCE: U-13212-4
<140> CURRENT APPLICATION NUMBER: 09/743885A
<141> CURRENT FILING DATE: 2001-01-16
<160> NUMBER OF SEQ ID NOS: 29
<170> SOFTWARE: PatentIn Ver. 2.1
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Tyr Lys Ile Tyr Lys Arg Lys Ser Ser Glu Gly Tyr Gln Ala Ile Pro
        35                  40                  45
Tyr Met Val Ala Leu Phe Ser Ala Gly Leu Leu Leu Tyr Tyr Ala Tyr
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Leu Arg Lys Asn Ala Tyr Leu Ile Val Ser Ile Asn Gly Phe Gly Cys
65                  70                  75                  80
Ala Ile Glu Leu Thr Tyr Ile Ser Leu Phe Leu Phe Tyr Ala Pro Arg
                85                  90                  95
Lys Ser Lys Ile Phe Thr Gly Trp Leu Met Leu Leu Glu Leu Gly Ala
            100                 105                 110
Leu Gly Met Val Met Pro Ile Thr Tyr Leu Leu Ala Glu Gly Ser His
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Arg Val Met Ile Val Gly Trp Ile Cys Ala Ala Ile Asn Val Ala Val
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68             180                 185                 190
70 Phe Pro Asn Ile Leu Gly Phe Leu Phe Gly Ile Val Gln Met Leu Leu
71         195                 200                 205
73 Tyr Phe Val Tyr Lys Asp Ser Lys Arg Ile Asp Asp Glu Lys Ser Asp
74     210                 215                 220
76 Pro Val Arg Glu Ala Thr Lys Ser Lys Glu Gly Val Glu Ile Ile Ile
77 225                 230                 235                 240
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99 <223> OTHER INFORMATION: FBP15 amino acid sequence
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106              20                  25                  30
108 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
109          35                  40                  45
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112      50                  55                  60
114 Thr Ile Asp Arg Tyr Lys Lys Ala Ser Ser Asp Ser Ser Asn Thr Gly
115  65                  70                  75                  80
117 Ser Thr Ser Glu Ala Asn Thr Gln Phe Tyr Gln Gln Glu Ala Ala Lys
118                  85                  90                  95
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121             100                 105                 110
123 Gly Glu Ser Leu Ser Ser Leu Thr Ala Lys Asp Leu Lys Gly Leu Glu
124         115                 120                 125
126 Thr Lys Leu Glu Lys Gly Ile Ser Arg Ile Arg Ser Lys Lys Asn Glu
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129 Leu Leu Phe Ala Glu Ile Glu Tyr Met Arg Lys Arg Glu Ile Asp Leu
130 145                 150                 155                 160
132 His Asn Asn Asn Gln Met Leu Arg Ala Lys Ile Ala Glu Ser Glu Arg
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135 Asn Val Asn Met Met Gly Gly Glu Phe Glu Leu Met Gln Ser His Pro
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138 Tyr Asp Pro Arg Asp Phe Phe Gln Val Asn Gly Leu Gln His Asn His
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183 cttcttggta atattgtatc attcatggtc ttcctagcac ccgtgccaac attttacaaa 180
184 atatataaaa ggaaatcatc agaaggatat caagcaatac catatatggt agcactgttc 240
185 agcgccggac tattgctata ttatgcttat ctcaggaaga atgcctatct tatcgtcagc 300
186 attaatggct ttggatgtgc cattgaatta acatatatct ctctgtttct cttttacgcg 360
187 cccagaaagt ctaagatttt cacagggtgg ctgatgctct tagaattggg agccctagga 420
188 atggtgatgc caattactta tttattagca gaaggctcac atagagtgat gatagtggga 480
189 tggatttgtg cagctatcaa tgttgctgtc tttgctgctc ctttaagcat catgaggcaa 540
190 gtaataaaaa caaagagtgt agagttcatg cccttcactt tatctttgtt cctcactctc 600
191 tgtgccacta tgtggttttt ctatgggttt ttcaagaagg acttttacat tgcgtttcca 660
192 aatatactgg gctttctatt cggaatcgtt caaatgctat tatattttgt ttacaaggat 720
193 tcaaagagaa tagatgatga aaaatctgat cctgttcgag aagctacaaa atcaaaagaa 780
194 ggtgtagaaa tcattatcaa cattgaagat gataattctg ataacgcatt gcagtccatg 840
195 gagaaggatt tttccagact gcggacatca aaataagcaa gaagatgatc aaaaaatgac 900
196 aaagctaagg agtttgaagt aaggcaagga acttgacact gaatatctaa gctaattagc 960
197 aagactttag cagcttgtaa tatttagtgt ttgtgaggtg ttaccttata attagcttgt 1020
198 agcatagcct tcccactaat aattctgctt agcgaatctt atatatggga aatacttaca 1080
199 ctagtatgca tcttctatat acatgtttgg cacttgacta tacatagaaa aattaacaag 1140
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205 <211> LENGTH: 1157
206 <212> TYPE: DNA

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207 <213> ORGANISM: Petunia x hybrida
209 <220> FEATURE:
210 <223> OTHER INFORMATION: strain: W115
212 <220> FEATURE:
213 <223> OTHER INFORMATION: tissue type: nectar gland
215 <220> FEATURE:
216 <223> OTHER INFORMATION: cDNA library of nectaries from Petunia hybrida
217 flowers
219 <220> FEATURE:
220 <223> OTHER INFORMATION: FBP15
222 <400> SEQUENCE: 5
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225 aataaagggg atgttccaga atcaagaaga gaagatgtca gactcgcctc agaggaagat 180
226 gggaagagga aagattgaga ttaagaggat tgaaaataca acaaatcgtc aagtcacttt 240
227 ctgtaagaga agaaatgggt tgcttaaaaa agcttatgaa ctttctgttc tttgtgatgc 300
228 tgaagttgct ctcatcgttt tctcaagccg tggccgcctc tatgaatatg ctaacaacag 360
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232 aaaagatctg aaaggcctgg agaccaaact tgagaaagga attagtagaa ttaggtccaa 600
233 aaagaatgaa ctcctgtttg ctgagattga gtatatgcga aaaagggaaa ttgatttgca 660
234 caacaacaat cagatgcttc gggcaaagat agctgagagt gaaagaaatg tgaacatgat 720
235 gggaggagaa tttgagctga tgcaatctca tccgtacgat ccaagagact tcttccaagt 780
236 gaacggctta cagcataatc atcaatatcc acgccaagac aacatggctc ttcaattagt 840
237 ataagtttat aataaaatgc atggtttgaa gcactctgat tgtggtggat ttggattatg 900
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239 agttcatcat ctctctcatc tatatgtctt aacaaaagtc ttagcttatg gactctaaaa 1020
240 caaagactta atttaacata taaatataat tgtgtaatgc tgttgtattg tatggtatgt 1080
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251 <221> NAME/KEY: sig_peptide
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261 <213> ORGANISM: Petunia x hybrida
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272 tatgaagagg accaagaagc tccaataatt ttgggaagag cattcttaat cacatcgatg 180
273 gcaattattg acatggaact tggggagatg actgtgagag cgcatggaga aaaggttact 240
274 ttcaaggttt ataataaaaa ggatcatatg gctaagtttg aagagtgttc tttgatagaa 300
275 tgtgtcagac gagaacatga aagtaaaccg aaagaggtgt ttgagcggaa tgtagaacaa 360
276 agtgaccacg gcacaataat tgacaagttg aaggaaaatt cacctaaagg aaggaagaag 420
277 acaaaagttc gtcgtaacaa gaggagacgt aaatgctgga agtgagctta aaggtgttgt 480
278 cgtactacga cgttaactaa ggcgcttgtc gggaggcaac cctagctttg tatgtaaatg 540
279 taaaagtaaa aaatatatat atagaaaaag gaaaatacaa aaagagtcgt gccgcgacgt 600
280 taaatcaagc gcttgttgga aggcaaccca atttttattg ttttagttgt tttacttatt 660
281 tagtattacg tagtttcttg ttgtttttgt agggctcggg actttcggaa ggtgaggtaa 720
282 tttcaaggca tcgcggtgtg tattgcagcg aggtaagtgt aagagttgag ttggaagcgt 780
283 ttggccaagt gttgcaccgt gagaggcttt caacctgttg cgacacgtga aaaattaaga 840
284 gccagatctg ctacattagc actgaagcat cgcttggcca atagcttgga atggaagcaa 900
285 gaattcaaac caaaatcaga aacgccacaa gagatgtgtc gcacactgca aagctttgtg 960
286 caaactagtg aacgcagaaa tagaaatgct acagcccatg cgtcgcttgg cttatggcag 1020
287 gcagcaaaaa ttcagcagca aaacagaaac gctgcgagaa acgcgtcgca tacgccatag 1080
288 ctttgtgtca aacagaacgt ccagaaattg aaaagctata agcctgcgtc gcttggctca 1140
289 tggcgtgcag actagaaaag ctctagcaga tgcgtcgcgt attgtatagc ttggtgtgaa 1200
290 acagaaagtt cgaaacttgg aaaacgataa cccagcgtcg cctcttcaac cgcgtccagg 1260
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293 atatatatat atatacacac acacaccatt tccagcgatc ttacctcatt tttattcaaa 1440
294 ccatttttct gcttcaaaag tttaaattat taatatgata agtcatccat agtcaaacaa 1500
295 gattttctat actattttgt cccttgtaat tttaaaaaaa aaatgagcga tggtaagata 1560
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301 tattattatt gctgtatttg tttgtcattt gaatttggca ccgcagattt ttgtatgcaa 1920
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303 tttatcatac tttaccgaat tcttgttttt tgtttctctg ttgttgttct ccactataaa 2040
304 taacatttgc agtgagtaaa gtttcttcag gtctcttttg tagattcaac aagagtattc 2100
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:17; N Pos. 9